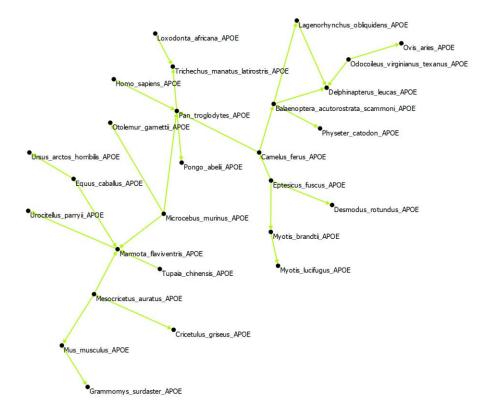
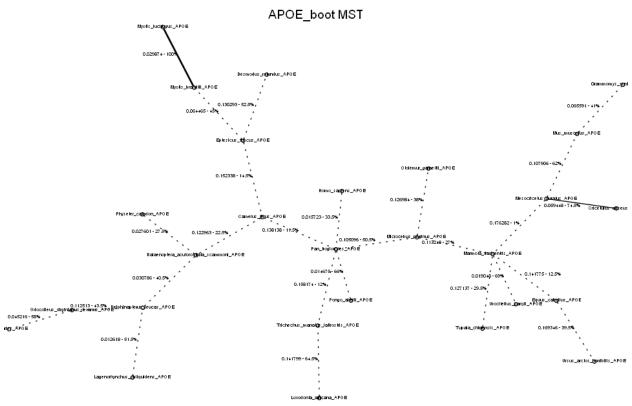
Consensus MST:





When running MSTGold on my data set, I used the same parameters shown in the textbook: MSTgold -f <filename> -m 300 -n 2000 and I got an output of only 2 unique MSTs. Amongst these two unique MSTs, when bootstrapped, both had the same bootstrap value of 42 with slightly different s.e. of +/- 4.5 for MST1 and +/- 5.3 for MST2.

Differences between Consensus MST & other Trees:

My consensus MST showed many similarities in groupings with the rest of my trees (excluding NJ) as well as my rooted network. However, using the MST we are unable to root our trees so the organization is a little bit different, which makes complete sense as the MST doesn't take any information other than direct changes into account. One disappointing part of my consensus MST is that because Graphviz doesn't seem to display the nodes very well, we are unable to easily visualize the distances that we gain from MSTgold.

Most Appropriate visualization:

I think that the most appropriate visualization for my current project would still be either my MP or ML trees as they sum up the hypothetical evolutionary information very well in an easy to read and digest manner. I think that either of those trees, along with their bootstrap and distance values would be best for me to determine a new possible model for studying APOE in animals.